

Supplemental Table 1: Thresholds, $-\log_{10}(p)$ threshold at a 0.05 FDR, for bin mapping the total number of dauer larvae, the population size and the percentage of dauer larvae.

Chromosome	Total number of dauer larvae	Population size	% dauer larvae
I	2.67	2.67	2.62
II	2.56	2.63	2.58
III	2.57	2.61	2.50
IV	2.89	2.59	2.66
V	2.94	2.86	3.02
X	2.80	2.61	2.65

Supplemental Table 2: Thresholds for the different mapping methods for total number of dauer larvae per chromosome.

Chromosome	BIN mapping $-\log_{10}(p)$ threshold at a 0.05 FDR	Single IL analysis threshold at a 0.05 Bonferroni correction (p)	Sequential IL analysis threshold at a 0.05 Bonferroni correction (p)
I	2.67	0.003	0.002
II	2.56	0.006	0.005
III	2.57	0.003	0.002
IV	2.89	0.003	0.002
V	2.94	0.004	0.003
X	2.80	0.004	0.003

Supplemental Table 3: Locations and effect of QTLs detected for the population size and the percentage of dauer larvae by analysis of individual ILs and by BIN mapping the ILs. Limits denote the maximum possible QTL region. ILs supporting the QTL are indicated in the last column, ILs in parentheses show the effect but don't meet the significance threshold.

Trait	Chr.	Limits (Mbp)	CB4856 effect	IL support	BIN support	ILs
Population size	X	0-1.5	-	X		078
	X	4.2-5.8	-	X		081
	X	5.8-8.0	-	X		081, 083, 084, 085
	X	12.9-14.6	-	X		088, 089, (090)
Percent dauer	I	1.9-3.5	+	X		002
	I	7.9-9.6	-	X	X	005, 006
	I	9.6-11.1	-	X		013
	I	11.1-15.0	-	X		016
	II	0-2.8	-	X		020
	II	11.2-13.2	+	X		025
	III	0-3.1	-		X	
	III	8.0-10.6	-	X		040
	IV	0.8-2.3	-	X		045, 048, (046)
	IV	2.3-3.9	-	X		053, (052)
	IV	12.7-16.4	-	(X)	X	(058, 059, 060)
	V	11.8-14.0	+	X		069, 071, 073
	V	17.4-19.5	-	X		075, 076
	X	0-2.4	-	X	X	078, 079, 081
	X	5.8-8.0	-	X	X	083, 085, 086, (084)
	X	12.9-17.6	+	X	X	089, (090)

Supplemental Table 4: QTLs identified by pairwise IL mapping. QTLs in bold meet both genome-wide and chromosome thresholds, QTLs in normal font meet chromosome threshold, and QTLs in italics are significant as single tests. For all QTLs, the effect size of the CB4856 allele is noted and the support for the QTL in the IL and BIN mapping is noted.

CHR	Left N2 marker	Limits (Mbp)	Right N2 marker	<i>p</i>	CB effect	Effect Size (CB4856)	ILs	CHR thresh.	GW thresh.	IL support	BIN support
I	1.9	2.8-7.9	8.7	2.00E-04	P	591	N2,02	X	X	X	X
I		4.3-8.7	9.6	5.00E-06	N	-792	04,06	X	X	X	X
<i>I</i>	<i>5.9</i>	<i>6.4-8.7</i>		<i>5.00E-03</i>	<i>P</i>	<i>320</i>	<i>13,08</i>				
I		8.7-10.3	11.1	2.00E-06	P	576	06,07	X	X		
<i>I</i>	<i>8.7</i>	<i>9.6-10.3</i>		<i>4.00E-03</i>	<i>N</i>	<i>-466</i>	<i>14,09</i>				
<i>I</i>	<i>9.6</i>	<i>10.3-10.3</i>	<i>11.1</i>	<i>7.00E-04</i>	<i>N</i>	<i>-391</i>	<i>N2;13</i>	<i>X</i>		<i>X</i>	
I		10.3-11.1	11.8	3.00E-05	P	603	13,14	X	X		
II		0-1.7	2.8	7.00E-08	N	-336	N2,19	X	X	X	
<i>II</i>		<i>0-2.8</i>	<i>3.4</i>	<i>3.00E-03</i>	<i>N</i>	<i>-117</i>	<i>23,22</i>	<i>X</i>			
II		1.7-2.8	3.4	4.00E-07	P	392	19,20	X	X		
<i>II</i>	<i>11.2</i>	<i>11.8-11.8</i>	<i>12.6</i>	<i>7.00E-03</i>	<i>P</i>	<i>147</i>	<i>N2,24</i>			<i>X</i>	
II		12.6-13.2	14.0	2.00E-04	N	-141	25,26	X	X	X	
II	13.2	14-14.8		1.00E-06	P	222	26,27	X	X		
III	2.5	3.1-8.3		2.00E-06	P	924	40,36	X	X		
III	8.0	8.3-10	1.6	3.00E-05	N	-742	N2,40	X	X	X	
III		10-10.6	11.3	8.00E-07	P	766	40,41	X	X		
IV		0-1.4	2.3	2.00E-04	N	-570	N2,45	X	X	X	X
IV	2.3	3.1-3.1	3.9	7.00E-05	N	-515	N2,53	X	X	X	
<i>IV</i>	<i>11.7</i>	<i>12.7-12.7</i>	<i>13.7</i>	<i>3.00E-03</i>	<i>N</i>	<i>-344</i>	<i>N2,59</i>			<i>X</i>	<i>X</i>
<i>V</i>		<i>5.8-13</i>	<i>14</i>	<i>3.00E-03</i>	<i>P</i>	<i>231</i>	<i>67,69</i>	<i>X</i>			<i>X</i>
V	10.4	10.9-17.4		1.00E-08	P	442	75,70	X	X		X
V	11.8	13-13	14	8.00E-06	P	332	N2,72	X	X	X	X
V	17.4	18.6-19.5		3.00E-04	N	-318	77,76	X	X		
<i>X</i>		<i>0-0.7</i>	<i>1.5</i>	<i>8.00E-03</i>	<i>N</i>	<i>-176</i>	<i>N2,78</i>			<i>X</i>	<i>X</i>
X		1.5-2.4	3.3	1.00E-04	P	238	79,80	X	X		
X		2.4-8.7	9.3	4.00E-06	N	-328	80,81	X	X		X
X	5.0	5.8-7.1	8	2.00E-05	N	-228	N2,83	X	X	X	X
<i>X</i>	<i>5.0</i>	<i>5.8-7.1</i>		<i>8.00E-04</i>	<i>P</i>	<i>161</i>	<i>85,84</i>	<i>X</i>			
X	5.8	7.1-8	8.7	3.00E-08	N	-306	N2,85	X	X	X	X
X	5.8	7.1-8.7	9.3	2.00E-04	N	-201	N2,86	X	X	X	X
<i>X</i>		<i>8-8.7</i>	<i>9.3</i>	<i>7.00E-04</i>	<i>P</i>	<i>105</i>	<i>85,86</i>	<i>X</i>			
X	8.7	9.3-10.3	11.1	9.00E-04	P	163	N2,87	X	X	X	
X	12.9	13.9-16.4	17.6	3.00E-07	N	-278	N2,89	X	X	X	X
<i>X</i>		<i>16.4-17.6</i>		<i>5.00E-03</i>	<i>P</i>	<i>120</i>	<i>89,90</i>				

Supplementary table 5: Analysis of dauer larvae formation in the *npr-1* mutants. Three models were used to explain the variation in total dauer number between the *npr-1* mutants, IL ewIR081 and N2. The models used are shown in the first row. The effect and the *p*-values of the individual components are shown in the respective columns.

Factor	Dauer~genotype		Dauer~genotype+batch		Dauer~genotype+batch+ population size	
	Effect	<i>p</i> -value	Effect	<i>p</i> -value	Effect	<i>p</i> -value
intercept	8822	<2e-16	6956	7e-15	2469	0.194
DA508	-3227	5e-5	-3281	3e-5	-3052	7e-5
DA609	-8181	<2e-16	-8211	<2e-16	-7737	<2e-16
DA650	-2412	2e-3	-2436	2e-3	-2329	2e-3
ewIR081	-8201	<2e-16	-7616	3e-15	-7478	4e-15
Batch	NA	NA	921	3e-3	1613	9e-5
Population size	NA	NA	NA	NA	5996	0.0098